

REMARKS

Introductory Comments

Reconsideration of the above-identified application in view of the foregoing arguments is respectfully requested.

Claims 52-81 are pending. Claims 62-69 and 71-76 remain withdrawn from consideration. Claims 52-61, 70 and 77-81 are under consideration.

Rejection of Claims 52-61, 70 and 77-81 Under 35 U.S.C. § 101

And § 112, First Paragraph

Claims 52-61, 70 and 77-81 are rejected under 35 U.S.C. § 101 and § 112, first paragraph, for the reason contained in the previous Office Action. The Examiner contends that the Declaration of Dr. Granados is germane to the rejection at issue and that it fails to provide any evidence that the BS322 polypeptides according to SEQ ID NOS: 25-28 are equivalent to the NY-BR-1 breast cancer antigen polypeptide. Applicants respectfully traverse this rejection.

As submitted by Applicants in their previous responses, the Dirk Jager et al. article “Identification of Tissue-specific Putative Transcription Factor...” support Applicants’ contention that SEQ ID NOS: 24-28 as claimed are useful as required by 35 U.S.C. § 101 and § 112, first paragraph. The Jager et al. article shows that the gene NY-BR-1 is one of the genes responsible for breast cancer. The gene has 37 exons. See the abstract. Applicants have shown in previous responses in Exhibit A, the 100% alignment match and homology between NY-BR-1 and a nucleotide sequence designated BS322 (SEQ ID NO: 9). Nucleotide sequence BS322 or SEQ ID NO: 9 as described in the instant specification, encodes the polypeptide sequences designated SEQ ID NOS: 24-28. These polypeptides are useful in the detection of breast disease which Examiner has refuted.

The Examiner contends in the previous Office Actions that the alignment match between BS322 and NY-BR-1 does not prove that BS322 is the same molecule as NY-BR-1 since 1143 nucleotides are unaccounted for. The Examiner uses this single basis to support her reason why SEQ ID NOS: 24-28 are not useful in the detection of breast disease. Although Applicants appreciate the Examiner’s detailed analysis, Applicants respectfully traverse the rejection and contend this line of reasoning is flawed for the reason set forth below.

Applicants agree with the Examiner’s observation that the alignment consensus between BS322 and NY-BR-1 does not prove BS322 is the exact same molecule of NY-BR-1. However, the 100% consensus between these two molecules over one thousand nucleotides indicates that BS322 could be a splice variant of NY-BR-1. Applicants have attached herein a portion of a BLAST result for AF269087 (NY-BR-1) versus the human genome. As the Examiner can see, the junctions of the exons for the gaps match those that are in the BS322 molecule. Specifically, three exons that account for gaps are at the positions of 3013-3200, 3197-4116 and 2796-3014. This information clearly provides evidence that BS322 is a splice variant of NY-BR-1.

As indicated in the Jager et al. article, NY-BR-1 comprises 37 exons. Exons, also known as expressed sequences, are defined as a portions of a gene

that appear in both the primary and mature mRNA transcripts (Fundamentals of Biochemistry, Voet *et al.*, John Wiley & Sons, Inc., 1999). Thus, one of ordinary skill in the art would recognize that although BS322 is not the exact molecule of NY-BR-1, the fact that there is a 100% consensus homology between the two molecules for over 1000 nucleotides of the exons indicates that one is a splice of another and would have significant commonalities. It is well known in the art that introns may be excluded from splices which maintain the functionality of a gene. An intron, also called an intervening sequence, is defined in the art as a part of a primary transcript, or DNA encoding it, that is removed by splicing during RNA processing and is not included in the mature, functional mRNA, rRNA or tRNA (Fundamentals of Biochemistry, Voet *et al.*, John Wiley & Sons, Inc., 1999).

As disclosed in the specification, SEQ ID NOS: 24-28 are derived from the BS322 molecule. As shown in Jager *et al.*, *supra*, and in Applicants' disclosure, mRNA expressions of the gene, i.e., sequence segments from the genes which encode proteins that have a specific epitope, are useful as markers for breast diseases. Thus, for these reasons, Applicants respectfully request the Examiner to withdraw the rejection of claims 52-61, 70 and 77- 35 under 35 U.S.C. § 101 and § 112, first paragraph, and allow the claims.

CONCLUSION

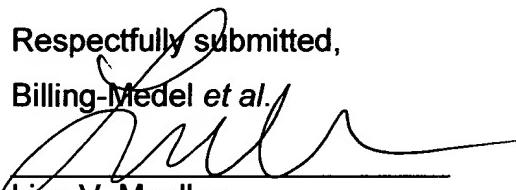
Applicants respectfully submit that the claims comply with the requirements of 35 U.S.C. Sections 101, 112, 102 and 103. Accordingly, a Notice of Allowance is believed in order and is respectfully requested.

Should the Examiner have any questions concerning the above, she is respectfully requested to contact the undersigned at the telephone number listed below. If the Examiner notes any further matters which the Examiner believes may be expedited by a telephone interview, the Examiner is requested to contact the undersigned.

If any additional fees are incurred as a result of the filing of this paper, authorization is given to charge deposit account no. 23-0785.

Respectfully submitted,

Billing-Medel et al.


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BS322 Contig summary1.TXT
Summary View of Contig "Contig[0013]"

>AF269087	#1	CTAGTCTATA CCAGCAACGA CTCCTACATC CTAGTCTATA CCAGCAACGA CTCCTACATC
>AF269087	#31	GTCCACTCTG GGGATCTTAG AAAGATCCAT GTCCACTCTG GGGATCTTAG AAAGATCCAT
>AF269087	#61	AAAGCTGCCT CCCGGGGACA AGTCCGGAAG AAAGCTGCCT CCCGGGGACA AGTCCGGAAG
>AF269087	#91	CTGGAGAAGA TGACAAAGAG GAAGAAGACC CTGGAGAAGA TGACAAAGAG GAAGAAGACC
>AF269087	#121	ATCAACCTTA ATATACAAGA CGCCCAGAAC ATCAACCTTA ATATACAAGA CGCCCAGAAC
>AF269087	#151	AGGACTGCTC TACACTGGGC CTGTGTCAAT AGGACTGCTC TACACTGGGC CTGTGTCAAT
>AF269087	#181	GGCCATGAGG AAGTAGTAAC ATTTCTGGTA GGCCATGAGG AAGTAGTAAC ATTTCTGGTA
>AF269087	#211	GACAGAAAGT GCCAGCTTGA CGTCCTTGAT GACAGAAAGT GCCAGCTTGA CGTCCTTGAT
>AF269087	#241	GGCGAACACA GGACACCTCT GATGAAGGCT GGCGAACACA GGACACCTCT GATGAAGGCT
>AF269087	#271	CTACAATGCC ATCAGGAGGC TTGTGCAAAT CTACAATGCC ATCAGGAGGC TTGTGCAAAT
>AF269087	#301	ATTCTGATAG ATTCTGGTGC CGATATAAAT ATTCTGATAG ATTCTGGTGC CGATATAAAT
>AF269087	#331	CTCGTAGATG TGTATGGCAA CATGGCTCTC CTCGTAGATG TGTATGGCAA CATGGCTCTC

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>AF269087	#361	CATTATGCTG TTTATAGTGA GATTTTGTCA CATTATGCTG TTTATAGTGA GATTTTGTCA
>AF269087	#391	GTGGTGGCAA AACTGCTGTC CCATGGTGCA GTGGTGGCAA AACTGCTGTC CCATGGTGCA
>AF269087	#421	GTCATCGAAG TGCAACAACAA GGCTAGCCTC GTCATCGAAG TGCAACAACAA GGCTAGCCTC
>AF269087	#451	ACACCACCTT TACTATCCAT AACGAAAAGA ACACCACCTT TACTATCCAT AACGAAAAGA
>AF269087	#481	AGTGAGCAA TTGTGGAATT TTTGCTGATA AGTGAGCAA TTGTGGAATT TTTGCTGATA
>AF269087	#511	AAAAATGCAA ATGCGAATGC AGTTAATAAG AAAAATGCAA ATGCGAATGC AGTTAATAAG
>AF269087	#541	TATAAATGCA CAGCCCTCAT GCTTGCTGTA TATAAATGCA CAGCCCTCAT GCTTGCTGTA
>AF269087	#571	TGTCATGGAT CATCAGAGAT AGTTGGCATG TGTCATGGAT CATCAGAGAT AGTTGGCATG
>AF269087	#601	CTTCTTCAGC AAAATGTTGA CGTCTTGCT CTTCTTCAGC AAAATGTTGA CGTCTTGCT
>AF269087	#631	GCAGATATAT GTGGAGTAAC TGCAGAACAT GCAGATATAT GTGGAGTAAC TGCAGAACAT
>AF269087	#661	TATGCTGTTA CTTGTGGATT TCATCACATT TATGCTGTTA CTTGTGGATT TCATCACATT
>AF269087	#691	CATGAACAAA TTATGGAATA TATACGAAAA CATGAACAAA TTATGGAATA TATACGAAAA
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>AF269087	#811	ACAGCTGAAA GCTTGGTGG AAAAAACACCT ACAGCTGAAA GCTTGGTGG AAAAAACACCT
>AF269087	#841	GATGAGGCTG CACCCTTGGT GGAAAGAAC GATGAGGCTG CACCCTTGGT GGAAAGAAC
>AF269087	#871	CCTGACACGG CTGAAAGCTT GGTGGAAAAA CCTGACACGG CTGAAAGCTT GGTGGAAAAA
>AF269087	#901	ACACCTGATG AGGCTGCATC CTTGGTGGAG ACACCTGATG AGGCTGCATC CTTGGTGGAG
>AF269087	#931	GGAACATCTG ACAAAATTCA ATGTTGGAG GGAACATCTG ACAAAATTCA ATGTTGGAG
>AF269087	#961	AAAGCGACAT CTGGAAAGTT CGAACAGTC AAAGCGACAT CTGGAAAGTT CGAACAGTC
>AF269087	#991	GCAGAAGAAA CACCTAGGGA AATTACGAGT GCAGAAGAAA CACCTAGGGA AATTACGAGT
>AF269087	#1021	CCTGCAAAAG AAACATCTGA GAAATTACG CCTGCAAAAG AAACATCTGA GAAATTACG
>AF269087	#1051	TGGCCAGCAA AAGGAAGACC TAGGAAGATC TGGCCAGCAA AAGGAAGACC TAGGAAGATC
>AF269087	#1081	GCATGGGAGA AAAAAGAAGA CACACCTAGG GCATGGGAGA AAAAAGAAGA CACACCTAGG
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	#1111	GAAATTATGA GTCCCGCAAA AGAAACATCT
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	#1201	ACACCTGTAA AGACTGGATG CGTGGCAAGA
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>AF269087	#1291	ACAAAAGAAT CATCTACAAA AGCAAGTGCC
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>AF269087	#1321	AATGATCAGA GGTTCCCATC AGAATCCAAA
	#1321	AATGATCAGA GGTTCCCATC AGAATCCAAA
>AF269087	#1351	CAAGAGGAAG ATGAAGAATA TTCTTGATGAT
	#1351	CAAGAGGAAG ATGAAGAATA TTCTTGATGAT
>AF269087	#1381	TCTCGGAGTC TCTTGAGAG TTCTGCAAAG
	#1381	TCTCGGAGTC TCTTGAGAG TTCTGCAAAG
>AF269087	#1411	ATTCAAGTGT GTATACCTGA GTCTATATAT
	#1411	ATTCAAGTGT GTATACCTGA GTCTATATAT
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>AF269087	#1501	AAGCCTGCCA TTGAAATGCA AAACTCTGTT
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	#1561	CAAACATTGA GAGCAGATCC GATGTTCCA
>AF269087	#1591	CCAGAATCCA AACAAAAGGA CTATGAAGAA
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>AF269087 >BS322 1 to 1198	#1981 #168 #1981	TCTTGGGATA CTGAGAGTCT CTGTGAGACT TCTTGGGATT CTGAGAGTCT CTGTGAGACT TCTTGGGATW CTGAGAGTCT CTGTGAGACT *
>AF269087 >BS322 1 to 1198	#2011 #198 #2011	GTTTCACAGA AGGATGTGTG TTTACCCAAG GTTTCACAGA AGGATGTGTG TTTACCCAAG GTTTCACAGA AGGATGTGTG TTTACCCAAG
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BS322 Contig summary1.TXT			
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>BS322 1 to 1198	#708	ATGGACATGC	AAACTTCAAAGCAGAGCCT
	#2521	ATGGACATGC	AAACTTCAAAGCAGAGCCT
>AF269087	#2551	CCCGAGAAC	CATCTGCCTT CGAGCCTGCC
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	#2611	GCCTTGAAT	TGAAGAATGA ACAAACATTG
>AF269087	#2641	AGAGCAGATC	AGATGTTCCC TTCAGAACATCA
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	#2641	AGAGCAGATC	AGATGTTCCC TTCAGAACATCA
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	#2671	AAACAAAAGA	ASGTTGAAGA AAATTCTTGG
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>AF269087	#2731	CAGAAGGATG	TGTGTGTACC CAAGGCTACA
>BS322 1 to 1198	#918	CAGAAGGATG	TGTGTGTACC CAAGGCTACA
	#2731	CAGAAGGATG	TGTGTGTACC CAAGGCTACA
>AF269087	#2761	CATCAAAAAG	AAATGGATAA AATAAGTGG
>BS322 1 to 1198	#948	CATCAAAAAG	AAATGGATAA AATAAGTGG
	#2761	CATCAAAAAG	AAATGGATAA AATAAGTGG
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>AF269087 >BS322 1 to 1198	#2821 #1008 #2821	ATCTTGGATA CAGTCATTC TTGTGAAAGA ATCTTGGATA CAATTCATTC TTGTGAAAGA ATCTTGGATA CARTTCATTC TTGTGAAAGA *
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>AF269087	#3121 #3121	GAAGTGAAAC AACAACTTGA ACAGGCTCTC GAAGTGAAAC AACAACTTGA ACAGGCTCTC

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>AF269087	#3151	AGAATACAAG ATATAGAATT GAAGAGTGTA AGAATACAAG ATATAGAATT GAAGAGTGTA
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>BS322 1199 to 2683 #13 >AF269087	#3211	CATGAAAATG AAAATTATCT CTTACATGAA CATGAAAATG AAAATTATCT CTTACATGAA CATGAAAATG AAAATTATCT CTTACATGAA
>BS322 1199 to 2683 #43 >AF269087	#3241	AATTGCATGT TGAAAAAGGA AATTGCCATG AATTGCATGT TGAAAAAGGA AATTGCCATG AATTGCATGT TGAAAAAGGA AATTGCCATG
>BS322 1199 to 2683 #73 >AF269087	#3271	CTAAAACCTGG AAATAGCCAC ACTGAAACAC CTAAAACCTGG AAATAGCCAC ACTGAAACAC CTAAAACCTGG AAATAGCCAC ACTGAAACAC
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>BS322 1199 to 2683 #133 >AF269087	#3331	GAGGACATTA AGATTTAAA AGAAAAGAAT GAGGACATTA AGATTTAAA AGAAAAGAAT GAGGACATTA AGATTTAAA AGAAAAGAAT
>BS322 1199 to 2683 #163 >AF269087	#3361	GCTGAACCTTC AGATGACCCCT AAAACTGAAA GCTGAACCTTC AGATGACCCCT AAAACTGAAA GCTGAACCTTC AGATGACCCCT AAAACTGAAA
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>BS322 1199 to 2683 #223 >AF269087	#3421	TATAGTGGGC AGCTTAAAGT TCTGATAGCT TATAGTGGGC AGCTTAAAGT TCTGATAGCT TATAGTGGGC AGCTTAAAGT TCTGATAGCT
>BS322 1199 to 2683 #253 >AF269087	#3451	GAGAACACAA TGCTCACTTC TAAATTGAAG GAGAACACAA TGCTCACTTC TAAATTGAAG

BS322 Contig summary1.TXT

>#3451 >BS322 1199 to 2683 #283 >AF269087 #3481 #3481 >BS322 1199 to 2683 #313 >AF269087 #3511 #3511 >BS322 1199 to 2683 #343 >AF269087 #3541 #3541 >BS322 1199 to 2683 #373 >AF269087 #3571 #3571 >BS322 1199 to 2683 #403 >AF269087 #3601 #3601 >BS322 1199 to 2683 #433 >AF269087 #3631 #3631 >BS322 1199 to 2683 #463 >AF269087 #3661 #3661 >BS322 1199 to 2683 #493 >AF269087 #3691 #3691 >BS322 1199 to 2683 #523 >AF269087 #3721 #3721 >BS322 1199 to 2683 #553 >AF269087 #3751 #3751	GAGAACACAA TGCTCACTTC TAAATTGAAG GAAAAACAAG ACAAAAGAAAT ACTAGAGGCA GAAAAACAAG ACAAAAGAAAT ACTAGAGGCA GAAAAACAAG ACAAAAGAAAT ACTAGAGGCA GAAATTGAAT CACACCATCC TAGACTGGCT GAAATTGAAT CACACCATCC TAGACTGGCT GAAATTGAAT CACACCATCC TAGACTGGCT TCTGCTGTAC AAGACCATGA TCAAATTGTG TCTGCTGTAC AAGACCATGA TCAAATTGTG TCTGCTGTAC AAGACCATGA TCAAATTGTG ACATCAAGAA AAAGTCAAGA ACCTGCTTTC ACATCAAGAA AAAGTCAAGA ACCTGCTTTC ACATCAAGAA AAAGTCAAGA ACCTGCTTTC CACATTGCAG GAGATGCTTG TTTGCAAAGA CACATTGCAG GAGATGCTTG TTTGCAAAGA CACATTGCAG GAGATGCTTG TTTGCAAAGA AAAATGAATG TTGATGTGAG TAGTACGATA AAAATGAATG TTGATGTGAG TAGTACGATA AAAATGAATG TTGATGTGAG TAGTACGATA TATAACAATG AGGTGCTCCA TCAACCACTT TATAACAATG AGGTGCTCCA TCAACCACTT TATAACAATG AGGTGCTCCA TCAACCACTT TCTGAAGCTC AAAGGAAATC CAAAAGCCTA TCTGAAGCTC AAAGGAAATC CAAAAGCCTA TCTGAAGCTC AAAGGAAATC CAAAAGCCTA AAAATTAATC TCAATTATGC AGGAGATGCT AAAATTAATC TCAATTATGC AGGAGATGCT AAAATTAATC TCAATTATGC AGGAGATGCT CTAAGAGAAA ATACATTGGT TTCAGAACAT CTAAGAGAAA ATACATTGGT TTCAGAACAT CTAAGAGAAA ATACATTGGT TTCAGAACAT
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BS322 Contig summary1.TXT

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>BS322 1199 to 2683 #613 >AF269087 #3811	CAAATGAAGG AAGCTGAACA CATGTATCAA CAAATGAAGG AAGCTGAACA CATGTATCAA CAAATGAAGG AAGCTGAACA CATGTATCAA
>BS322 1199 to 2683 #643 >AF269087 #3841	AACGAACAAG ATAATGTGAA CAAACACACT AACGAACAAG ATAATGTGAA CAAACACACT AACGAACAAG ATAATGTGAA CAAACACACT
>BS322 1199 to 2683 #673 >AF269087 #3871	GAACAGCAGG AGTCTCTAGA TCAGAAATT GAACAGCAGG AGTCTCTAGA TCAGAAATT GAACAGCAGG AGTCTCTAGA TCAGAAATT
>BS322 1199 to 2683 #703 >AF269087 #3901	TTTCAACTAC AAAGCAAAAA TATGTGGCTT TTTCAACTAC AAAGCAAAAA TATGTGGCTT TTTCAACTAC AAAGCAAAAA TATGTGGCTT
>BS322 1199 to 2683 #733 >AF269087 #3931	CAACAGCAAT TAGTCATGC ACATAAGAAA CAACAGCAAT TAGTCATGC ACATAAGAAA CAACAGCAAT TAGTCATGC ACATAAGAAA
>BS322 1199 to 2683 #763 >AF269087 #3961	GCTGACAACA AAAGCAAGAT ACAATTGAT GCTGACAACA AAAGCAAGAT ACAATTGAT GCTGACAACA AAAGCAAGAT ACAATTGAT
>BS322 1199 to 2683 #793 >AF269087 #3991	ATTCATTTTC TTGAGAGGAA AATGCAACAT ATTCATTTTC TTGAGAGGAA AATGCAACAT ATTCATTTTC TTGAGAGGAA AATGCAACAT
>BS322 1199 to 2683 #823 >AF269087 #4021	CATCTCCTAA AAGAGAAAAA TGAGGAGATA CATCTCCTAA AAGAGAAAAA TGAGGAGATA CATCTCCTAA AAGAGAAAAA TGAGGAGATA
>BS322 1199 to 2683 #853 >AF269087 #4051	TTTAATTACA ATAACCATT AAAAACCGT TTTAATTACA ATAACCATT AAAAACCGT TTTAATTACA ATAACCATT AAAAACCGT
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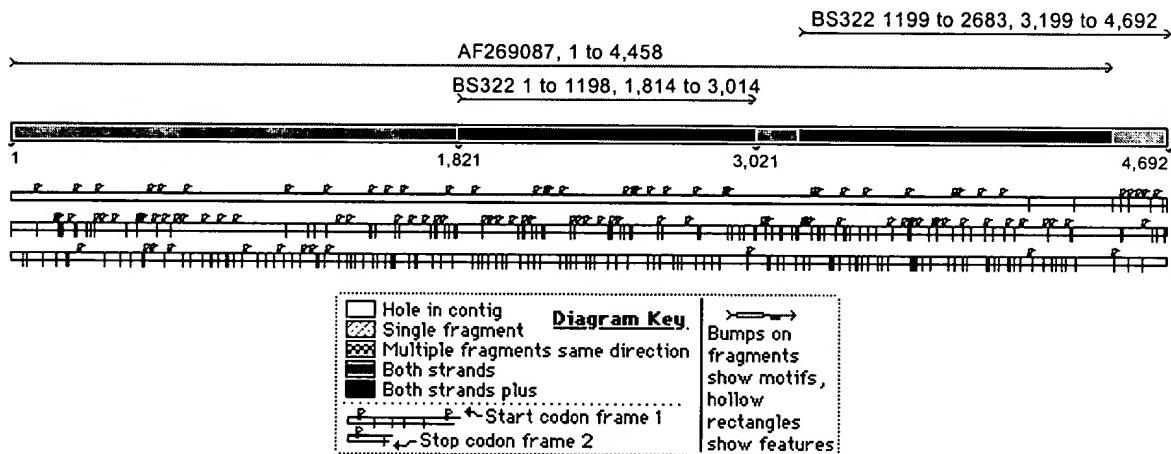
BS322 Contig summary1.TXT

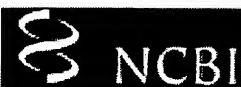
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#4111	
#4111	
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#4141	
#4141	
>BS322 1199 to 2683 #973 >AF269087	TCTTTACTCA CAACTCATGC TAGGAGGCCA TCTTTACTCA CAACTCATGC TAGGAGGCCA TCTTTACTCA CAACTCATGC TAGGAGGCCA
#4171	
#4171	
>BS322 1199 to 2683 #1003 >AF269087	GTCCTAGCAT CACCTTATGT TGAAAATCTT GTCCTAGCAT CACCTTATGT TGAAAATCTT GTCCTAGCAT CACCTTATGT TGAAAATCTT
#4201	
#4201	
>BS322 1199 to 2683 #1033 >AF269087	ACCAATAGTC TGTGTCAACA GAATACTTAT ACCAATAGTC TGTGTCAACA GAATACTTAT ACCAATAGTC TGTGTCAACA GAATACTTAT
#4231	
#4231	
>BS322 1199 to 2683 #1063 >AF269087	TTTAGAAGAA AAATTCTATGA TTTCTTCCTG TTTAGAAGAA AAATTCTATGA TTTCTTCCTG TTTAGAAGAA AAATTCTATGA TTTCTTCCTG
#4261	
#4261	
>BS322 1199 to 2683 #1093 >AF269087	AAGCCTACAG ACATAAAATA ACAGTGTGAA AAGCCTACAG ACATAAAATA ACAGTGTGAA AAGCCTACAG ACATAAAATA ACAGTGTGAA
#4291	
#4291	
>BS322 1199 to 2683 #1123 >AF269087	GAATTACTTG TTCACGAA:T :C:TCGCTCT GAATTACTTG TTCACGAAATT GCATAAAGCT GAATTACTTG TTCACGAAATT GCATMRMKCT * * * ***
#4321	
#4321	
>BS322 1199 to 2683 #1153 >AF269087	GCACCTCCA:G CCTAGGGGCC TAGTGAAACC GCACAGGATT CCCATCTACC CTGATGATGC GCACWSSATK CCYAKSYRCC YWGWKRAWSC *** ** * *** ** *** *** **
#4351	
#4351	
>BS322 1199 to 2683 #1183 >AF269087	CTGTGTCA:A AAAGAAAA:A AACAAAAAAC AGCAGACATC ATTCAATCCA ACCAGAATCT MKSWGWCATM AWWSAAWMCA AMCARAACW **** * ** *** *** * * * *
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#4381	

BS322 Contig summary1.TXT

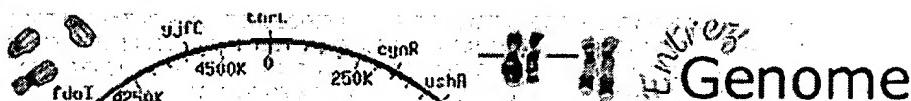
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>BS322 1199 to 2683 #1243 >AF269087	#4441	GAGACCCTGT ATCACTTCAA ATAATGTGTT GAGACTCCAC CTCGGAAA GAGACYCYRY MTCRSWWMAA ATAATGTGTT * *** * *****
>BS322 1199 to 2683 #1273	#4471	AAACAAGCAT CTTCATCTCA TTAAATAGAA AAACAAGCAT CTTCATCTCA TTAAATAGAA
>BS322 1199 to 2683 #1303	#4501	ATGTTGAAAA ATTGCTTTG GAATAATTGA ATGTTGAAAA ATTGCTTTG GAATAATTGA
>BS322 1199 to 2683 #1333	#4531	CTTATGGATA TTTCATCAA TTTACAGTTG CTTATGGATA TTTCATCAA TTTACAGTTG
>BS322 1199 to 2683 #1363	#4561	GCTATGCTTT CTTATTGTGC ATACTATGAA GCTATGCTTT CTTATTGTGC ATACTATGAA
>BS322 1199 to 2683 #1393	#4591	ATGTTTTCT TCAAAAAGTG TTTATAAGTG ATGTTTTCT TCAAAAAGTG TTTATAAGTG
>BS322 1199 to 2683 #1423	#4621	GTAAGTTAA GAATGGGTT GACAGCATTA GTAAGTTAA GAATGGGTT GACAGCATTA
>BS322 1199 to 2683 #1453	#4651	TCTTTTGTTG TTATTTGATT AAACATTAC TCTTTTGTTG TTATTTGATT AAACATTAC
>BS322 1199 to 2683 #1483	#4681	TAATTGTGCA TA

1. BS 322 contains 2683 nucleotides. This sequence was obtained by sequencing Incyte clone 4304443 in house.
2. NY-BR-1 (AF269087) contains 4466 nucleotides.
3. The contig (**below**) shows that BS322 is missing a single stretch of 185 nucleotides that are present in NY-BR-1. These nucleotides are missing between position 1198 and 1199 of BS322. The missing piece is nucleotides 3015 thru 3198 of NY-BR-1(AF269087). The first 45 bases of BS322 are a poor match to AF269087). The remaining bases are almost 100% identical. See BS322 contig summary file.
4. It appears that Incyte clone 4304443 is a splice variant of NY-BR-1. The gap occurs in the open reading frame region.
5. The primers used for the NY-BR-1 study were: Forward 2181 to 2202 and Reverse 3088 to 3111(AF269087). These primers are contained within BS322.





results of BLAST



BLASTN 2.2.6 [Apr-09-2003]

RID: 1058379474-018463-9635

Database: contig
545 sequences; 2,866,452,029 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

Show positions of the BLAST hits in the human genome using the Entrez Genomes MapViewer

Query= gi|13469728|gb|AF269087.1|AF269087 Homo sapiens breast cancer antigen NY-BR-1 mRNA, complete cds.
(4458 letters)

Distribution of 115 Blast Hits on the Query Sequence

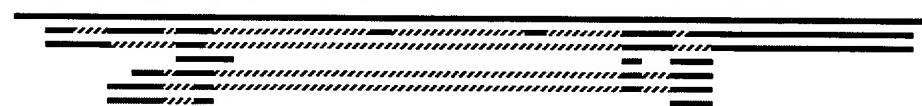
Mouse-over to show defline and scores. Click to show alignments

Color Key for Alignment Scores

<40 40-50 50-80 80-200 >200

1_2991

0 500 1000 1500 2000 2500 3000 3500 4000



Sequences producing significant alignments:

Score E
(bits) Value

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ref NT_011512.8 Hs21_11669	Homo sapiens chromosome 21 genome...	1319	0.0
ref NT_033985.5 Hs10_34140	Homo sapiens chromosome 10 genome...	1165	0.0
ref NT_011387.8 Hs20_11544	Homo sapiens chromosome 20 genome...	262	2e-66
ref NT_005058.13 Hs2_5215	Homo sapiens chromosome 2 genomic...	235	2e-58
ref NT_024983.9 Hs18_25139	Homo sapiens chromosome 18 genome...	202	1e-48
ref NT_078061.1 Hs9_78130	Homo sapiens chromosome 9 genomic...	192	1e-45
ref NT_078059.1 Hs9_78128	Homo sapiens chromosome 9 genomic...	192	1e-45
ref NT_037852.3 Hs15_37856	Homo sapiens chromosome 15 genome...	167	3e-38
ref NT_028395.2 Hs22_28554	Homo sapiens chromosome 22 genome...	127	5e-26

Alignments

Query: 3977 agataacaattgatattcatttctttagagggaaaatgcaacatcatctcctaaaagaga 4036
| |||||||
Sbjct: 19484019 agataacaattgatattcatttctttagagggaaaatgcaacatcatctcctaaaagaga 19484078

Query: 4037 aaaatgaggagatattaattacaataaccattaaaaaccgtatatcaatatgaaa 4096
| |||||||
Sbjct: 19484079 aaaatgaggagatattaattacaataaccattaaaaaccgtatatcaatatgaaa 19484138

Query: 4097 aagagaaagcagaaacagaa 4116
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Identities = 576/576 (100%)
Strand = Plus / Plus

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| |||||||
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| |||||||
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Query: 869 cacctgacacggctgaaagcttggggaaaaaacacctgatgaggctgcacccttggg 928
| |||||||
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Query: 929 agggAACATCTGACAAAATTCAATGTTGGAGAAAGCGACATCTGGAAAGTCTGAACAGT 988
| |||||||
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Query: 989 cagcagaagaaacaccttagggaaattacgagtccctgcaaaagaaacatctgagaaattta 1048
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Query: 1289 ctacaaaagaatcatctacaaaagcaagtgccaatg 1324
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Sbjct: 19406515 ctacaaaagaatcatctacaaaagcaagtgccatg 19406550

Score = 423 bits (220), Expect = e-115
Identities = 220/220 (100%)
Strand = Plus / Plus

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|||||||
Sbjct: 19495722 aactcatqagaqacaaqcqataqaaaacttctttqqqaaaacaaacaqaccqatctta 19495781

Query: 4177 ctcacaactcatgtctaggaggccagtccatcaccttatgttaaaaatcttaccaat 4236
||| ||| ||| ||| ||| ||| |||
Sbjct: 19495782 ctcacaactcatgtctaggaggccagtccatcaccttatgttaaaaatcttaccaat 19495841

Query: 4237 agtctgtgtcaacagaatacttatttagaaaaattcatgattcttcgtaaaggcct 4296
||| ||| ||| ||| ||| |||
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Query: 4297 acagacataaaataacagtgtgaagaattacttgttcacg 4336
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Score = 415 bits (216), Expect = e-113
Identities = 219/220 (99%), Gaps = 1/220 (0%)
Strand = Plus / Plus

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Sbjct: 19480436 aqacaqatccaactaqcctatcaaaaatcttgatacagttcatttctgtgaaagagcaa 19480495

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||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 19480496 gggaaacttcaaaaagatcactgtgaacaacgtacaggaaaaatggAACAAatggaaaaaga 19480555

Query: 2915 agttttgttactgaaaaagaaaactgtcagaagcaaaagaataaaatcacagtttagaga 2974
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Sbjct: 19480556 agttttgttactgaaaaagaaaactgtcagaagcaaaagaataaaatcacagtttagaga 19480615

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Strand = Plus / Plus

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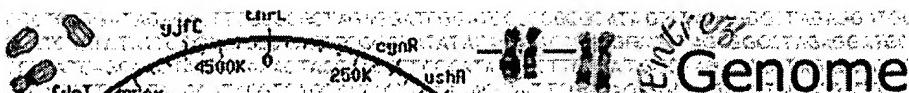
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Query: 3193 aatcaggt 3200
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Sbjct: 19482134 aatcaggt 19482141



results of BLAST



BLASTN 2.2.6 [Apr-09-2003]

RID: 1058379474-018463-9635

Database: contig
545 sequences; 2,866,452,029 total letters

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Show positions of the BLAST hits in the human genome using the Entrez Genomes MapViewer

Query= gi|13469728|gb|AF269087.1|AF269087 Homo sapiens breast cancer antigen NY-BR-1 mRNA, complete cds.
(4458 letters)

Distribution of 115 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments

Color Key for Alignment Scores

<40 40-50 50-80 80-200 >200

1_2991

0 500 1000 1500 2000 2500 3000 3500 4000



Sequences producing significant alignments:

Score E
(bits) Value

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ref NT_033985.5 Hs10_34140	Homo sapiens chromosome 10 genomic...	1165	0.0
ref NT_011387.8 Hs20_11544	Homo sapiens chromosome 20 genomic...	262	2e-66
ref NT_005058.13 Hs2_5215	Homo sapiens chromosome 2 genomic...	235	2e-58
ref NT_024983.9 Hs18_25139	Homo sapiens chromosome 18 genomic...	202	1e-48
ref NT_078061.1 Hs9_78130	Homo sapiens chromosome 9 genomic...	192	1e-45
ref NT_078059.1 Hs9_78128	Homo sapiens chromosome 9 genomic...	192	1e-45
ref NT_037852.3 Hs15_37856	Homo sapiens chromosome 15 genomic...	167	3e-38
ref NT_028395.2 Hs22_28554	Homo sapiens chromosome 22 genomic...	127	5e-26

Alignments

Query: 3977 agataacaattgatattcatttctttagagggaaatgcacatcatctcctaaaagaga 4036
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Score = 1108 bits (576), Expect = 0.0
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Strand = Plus / Plus

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Query: 869 cacctgacacggctgaaAGCTTGGTGGAAAAAACACCTGATGAGGCTGCATCCTGGTGG 928
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Query: 929 agggAACATCTGACAAAATTCAATGTTGGAGAAAGCGACATCTGGAAAGTTCGAACAGT 988
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Score = 423 bits (220), Expect = e-115
Identities = 220/220 (100%)
Strand = Plus / Plus

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Score = 415 bits (216), Expect = e-113
Identities = 219/220 (99%), Gaps = 1/220 (0%)
Strand = Plus / Plus

Query: 2796 aga-agattcaactagcctatcaaaaatcttgatcacagttcatttgtgaaagagcaa 2854
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 19480436 aqacaqattcaactaqcctatcaaaaatcttqatacacagttcatttgtqaaaqqaqcaa 19480495

Query: 2855 gggaaacttcaaaaagatcactgtgaacaacgtacaggaaaaatggAACAAATgaaaaaga 2914
|||||||
Sbjct: 19480496 gggaaacttcaaaaagatcactgtgaacaacgtacaggaaaaatggAACAAATgaaaaaga 19480555

Query: 2915 agttttgtgtactaaaaaaaactgtcagaagcaaaagaataaaatcacagtttagaga 2974
||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 19480556 atttttatatactaaaaaaaactgtcagaagcaaaagaataaaatcacagtttagaga 19480615

Query: 2975 accaaaaaggtaatggaaacaagagctctgcagtgtgag 3014
|||||||
Sbjct: 19480616 accaaaaaggtaatggaaacaagagctctgcagtgtgag 19480655

Score = 362 bits (188), Expect = 1e-96
Identities = 188/188 (100%)
Strand = Plus / Plus

Query: 3013 agattgactttaaccagaagaagagaagaaaatgccatatattaaatgaaaaa 3072
|||||||
Sbjct: 19481954 agattgactttaaccagaagaagagaagaaaatgccatatattaaatgaaaaa 19482013

Query: 3073 attagggaaagaatttaggaagaatcgaaaggcgcgcataggaaagaggtaaagtgtaaaacaa 3132

Sbjct: 19482014 attagggagaatttaggaagaatcgaaggagcgcattggaaaagaggttagaagtaaaacaa 19482073

Query: 3133 caacttgaacaggctctcagaatacagaattgaagagtgttagaaagtatgg 3192

Shict: 19482074 caacttggaaaggctctcagaatacaagatataagaatttaaaggatgttagaaaagtaatttg 19482133

Query: 3193 aatccagg 3200